

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/619,992 A  
Source: IFW16  
Date Processed by STIC: 12/06/2005

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IFW16

**RAW SEQUENCE LISTING** DATE: 12/06/2005  
**PATENT APPLICATION:** US/10/619,992A TIME: 13:09:50

Input Set : D:\00-617-F.ST25.txt  
Output Set: N:\CRF4\12062005\J619992A.raw

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3 <110> APPLICANT: Oregon Health & Science University
4     Hefeneider, Steven
5     Bennett, Robert
6     Seiss, Donald
7     Merkins, Louise
9 <120> TITLE OF INVENTION: Mammalian Cell Surface DNA Receptor
11 <130> FILE REFERENCE: 00-617-F
13 <140> CURRENT APPLICATION NUMBER: US 10/619992A
14 <141> CURRENT FILING DATE: 2003-07-15
16 <150> PRIOR APPLICATION NUMBER: 09/921,099
17 <151> PRIOR FILING DATE: 2001-08-01
19 <160> NUMBER OF SEQ ID NOS: 21
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 4351
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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30 <221> NAME/KEY: CDS
31 <222> LOCATION: (602)..(4174)
33 <400> SEQUENCE: 1
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38 tattatgttt tgggttactg gtatccaag gaaaaacactt tttaaacaaa caaaacaaaa   180
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42 tgcttggttt atgtggcgt tgagaaaaat acataaaagc tttatgtttt attatgttag 300
44 caaccaatat aaatacagtt tagttgaaag gaacactatt aaggtattgt ttccaggcag 360
46 aatttcagaa atgtattaa ttccagaaat aggtttta aaaaagacat ccaaaggta 420
48 taaaattatt tagaagtatt tttaggtctga agctgtataa gttgacttaa gcaattaact 480
50 cttcaaaggta gaatgtgaa tatgtggta attcatactt ttgtccattt ctatgttaca 540
52 aaacactaca cagcaaaaata atgatctgct agactgctaa cccgagcatc cagttccac 600
54 a atg cct gtg cag gca gct caa tgg aca gaa ttt ctg tcc tgt cca atc 649
55 Met Pro Val Gln Ala Ala Gln Trp Thr Glu Phe Leu Ser Cys Pro Ile
56   1           5           10          15
58 tgc tat aat gaa ttt gat gag aat gtg cac aaa ccc atc agt tta ggt      697
59 Cys Tyr Asn Glu Phe Asp Glu Asn Val His Lys Pro Ile Ser Leu Gly
60       20          25          30
62 tgt tca cac act gtt tgc aag acc tgc ttg aat aaa ctt cat cga aaa      745
63 Cys Ser His Thr Val Cys Lys Thr Cys Leu Asn Lys Leu His Arg Lys
64       35          40          45
66 gct tgt cct ttt gac cag act gcc atc aac aca gat att gat gta ctt      793
67 Ala Cys Pro Phe Asp Gln Thr Ala Ile Asn Thr Asp Ile Asp Val Leu
68       50          55          60

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74	cat	cag	tca	att	aag	tta	agt	aat	cta	ggg	gag	aat	aaa	cac	tat	gag		889	
75	His	Gln	Ser	Ile	Lys	Leu	Ser	Asn	Leu	Gly	Glu	Asn	Lys	His	Tyr	Glu			
76						85				90				95					
78	gtt	gca	aag	aaa	tgc	gtt	gag	gat	ttg	gca	ctc	tac	tta	aaa	cca	cta		937	
79	Val	Ala	Lys	Lys	Cys	Val	Glu	Asp	Leu	Ala	Leu	Tyr	Leu	Lys	Pro	Leu			
80						100				105				110					
82	agt	gga	ggg	aaa	ggg	gtt	gta	gct	agc	ttg	aac	cag	agt	gca	ctg	agc	cgt	985	
83	Ser	Gly	Gly	Lys	Gly	Val	Ala	Ser	Leu	Asn	Gln	Ser	Ala	Leu	Ser	Arg			
84						115				120				125					
86	cca	atg	caa	agg	aaa	ctg	gtg	aca	ctt	gta	aac	tgt	caa	ctg	gtg	gag		1033	
87	Pro	Met	Gln	Arg	Lys	Leu	Val	Thr	Leu	Val	Asn	Cys	Gln	Leu	Val	Glu			
88						130				135				140					
90	gaa	gaa	ggg	cgt	gtt	gta	aga	gcc	atg	cga	gca	gct	cgt	tcc	ctt	gga	gaa	1081	
91	Glu	Glu	Gly	Arg	Val	Arg	Ala	Met	Arg	Ala	Ala	Arg	Ser	Leu	Gly	Glu			
92	145					150				155				160					
94	aga	act	gta	aca	gaa	ctg	ata	tta	cag	cac	cag	aac	cct	cag	cag	ttg		1129	
95	Arg	Thr	Val	Thr	Glu	Leu	Ile	Leu	Gln	His	Gln	Asn	Pro	Gln	Gln	Leu			
96						165				170				175					
98	tct	gcc	aat	cta	tgg	gcc	gct	gtc	agg	gct	cga	gga	tgc	cag	ttt	tta		1177	
99	Ser	Ala	Asn	Leu	Trp	Ala	Ala	Val	Arg	Ala	Arg	Gly	Cys	Gln	Phe	Leu			
100						180				185				190					
102	ggg	cca	gct	atg	caa	gaa	gag	gcc	ttg	aag	ctg	gtg	tta	ctg	gca	tta		1225	
103	Gly	Pro	Ala	Met	Gln	Glu	Glu	Ala	Leu	Lys	Leu	Val	Leu	Leu	Ala	Leu			
104						195				200				205					
106	gaa	gat	ggg	tct	gcc	ctc	tca	agg	aaa	gtt	ctg	gta	ctt	ttt	gtt	gtg		1273	
107	Glu	Asp	Gly	Ser	Ala	Leu	Ser	Arg	Lys	Val	Leu	Val	Leu	Phe	Val	Val			
108						210				215				220					
110	cag	aga	cta	gaa	cca	aga	ttt	cct	cag	gca	tca	aaa	aca	agt	att	ggg		1321	
111	Gln	Arg	Leu	Glu	Pro	Arg	Phe	Pro	Gln	Ala	Ser	Lys	Thr	Ser	Ile	Gly			
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114	cat	gtt	gtg	caa	cta	ctg	tat	cga	gct	tct	tgt	ttt	aag	gtt	acc	aaa		1369	
115	His	Val	Val	Gln	Leu	Leu	Tyr	Arg	Ala	Ser	Cys	Phe	Lys	Val	Thr	Lys			
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119	Arg	Asp	Glu	Asp	Ser	Ser	Leu	Met	Gln	Leu	Lys	Glu	Glu	Phe	Arg	Ser			
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122	tat	gaa	gca	tta	cgc	aga	gaa	cat	gtt	gcc	caa	att	gtt	cat	att	gcc		1465	
123	Tyr	Glu	Ala	Leu	Arg	Arg	Glu	His	Asp	Ala	Gln	Ile	Val	His	Ile	Ala			
124						275				280				285					
126	atg	gaa	gca	gga	ctc	cgt	att	tca	cct	gaa	cag	tgg	tcc	tct	ctt	ttg		1513	
127	Met	Glu	Ala	Gly	Leu	Arg	Ile	Ser	Pro	Glu	Gln	Trp	Ser	Ser	Leu	Leu			
128						290				295				300					
130	tat	ggg	gtt	gat	ttg	gct	cat	aaa	tca	cac	atg	cag	tct	atc	att	gat	aag		1561
131	Tyr	Gly	Asp	Glu	Leu	Ala	His	Lys	Ser	His	Met	Gln	Ser	Ile	Ile	Asp	Lys		
132	305					310				315				320					
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140				340					345					350		
142	cat	tta	gag	ctt	ctt	gca	aac	ata	gac	cct	aat	cca	gac	gct	gtt	tca
143	His	Leu	Glu	Leu	Leu	Ala	Asn	Ile	Asp	Pro	Asn	Pro	Asp	Ala	Val	Ser
144				355					360					365		
146	cca	act	tgg	gag	cag	ctg	gaa	aat	gca	atg	gta	gct	gtt	aaa	aca	gta
147	Pro	Thr	Trp	Glu	Gln	Leu	Glu	Asn	Ala	Met	Val	Ala	Val	Lys	Thr	Val
148				370					375					380		
150	gtt	cat	ggc	ctt	gtg	gac	ttc	ata	caa	aat	tat	agt	aga	aaa	ggc	cat
151	Val	His	Gly	Leu	Val	Asp	Phe	Ile	Gln	Asn	Tyr	Ser	Arg	Lys	Gly	His
152	385				390				395					400		
154	gag	acc	cct	cag	cag	ccg	aaa	ttt								
155	Glu	Thr	Pro	Gln	Pro	Gln	Pro	Asn	Ser	Lys	Tyr	Lys	Thr	Ser	Met	Cys
156					405				410					415		
158	cga	gat	ttg	cga	cag	cag	ggg									
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160					420				425					430		
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163	Phe	Ala	His	Ser	Gln	Glu	Glu	Leu	Glu	Lys	Tyr	Arg	Leu	Arg	Asn	Lys
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166	aag	atc	aat	gcc	act	gtt	aga	acg	ttt	cct	ttt	cta	aat	aaa	gtt	ggt
167	Lys	Ile	Asn	Ala	Thr	Val	Arg	Thr	Phe	Pro	Leu	Leu	Asn	Lys	Val	Gly
168					450				455					460		
170	gtt	aac	aac	act	gtc	aca	acc	aca	gcc	gga	aat	gtc	att	tct	gtc	ata
171	Val	Asn	Asn	Thr	Val	Thr	Thr	Thr	Ala	Gly	Asn	Val	Ile	Ser	Val	Ile
172	465				470				475					480		
174	gga	agt	act	gaa	aca	aca	ggg	aaa	att	gtt	cca	agt	aca	aac	gga	att
175	Gly	Ser	Thr	Glu	Thr	Thr	Gly	Lys	Ile	Val	Pro	Ser	Thr	Asn	Gly	Ile
176					485				490					495		
178	tca	aat	gca	gaa	aac	agt	gtt	tcc	cag	cta	atc	tca	cgt	agt	act	gac
179	Ser	Asn	Ala	Glu	Asn	Ser	Val	Ser	Gln	Leu	Ile	Ser	Arg	Ser	Thr	Asp
180					500				505					510		
182	agt	acc	tta	aga	gct	ctg	gag	acc	gtt	aaa	gtt	gga	aag	gtt	ggc	
183	Ser	Thr	Leu	Arg	Ala	Leu	Glu	Thr	Val	Lys	Lys	Val	Gly	Lys	Val	Gly
184					515				520					525		
186	gct	aat	gtt	cag	aat	gtt	gct	ggg	ccc	tct	gca	aat	tct	gtt	act	gaa
187	Ala	Asn	Gly	Gln	Asn	Ala	Ala	Gly	Pro	Ser	Ala	Asp	Ser	Val	Thr	Glu
188					530				535					540		
190	aat	aaa	att	ggt	tct	cca	ccc	aag	act	cct	gta	agt	aat	gta	gca	gct
191	Asn	Lys	Ile	Gly	Ser	Pro	Pro	Lys	Thr	Pro	Val	Ser	Asn	Val	Ala	Ala
192	545				550				555					560		
194	acc	tca	gct	ggg	ccc	tct	aat	gtt	gga	aca	gag	ctg	aat	tct	gtg	cct
195	Thr	Ser	Ala	Gly	Pro	Ser	Asn	Val	Gly	Thr	Glu	Leu	Asn	Ser	Val	Pro
196					565				570					575		
198	caa	aaa	tcc	agc	cca	ttt	cta	act	aga	gtt	cca	gtt	tat	cct	ccg	cat
199	Gln	Lys	Ser	Ser	Pro	Phe	Leu	Thr	Arg	Val	Pro	Val	Tyr	Pro	Pro	His

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206	gaa gtc cca cag tac cca cag aca gga tac tat cca cca cct cca acg			2473
207	Glu Val Pro Gln Tyr Pro Gln Thr Gly Tyr Tyr Pro Pro Pro Pro Thr			
208	610	615	620	
210	gta cca gct ggt gtg gct ccc tgt gtt cct cgc ttt gtg agg tcc aat			2521
211	Val Pro Ala Gly Val Ala Pro Cys Val Pro Arg Phe Val Arg Ser Asn			
212	625	630	635	640
214	aac gtt cca gag tcc tcc ctc cca cct gct tcc atg cca tat gcc gat			2569
215	Asn Val Pro Glu Ser Ser Leu Pro Pro Ala Ser Met Pro Tyr Ala Asp			
216	645	650	655	
218	cat tac agt aca ttt tcc cct cga gat cga atg aat tct tct cct tac			2617
219	His Tyr Ser Thr Phe Ser Pro Arg Asp Arg Met Asn Ser Ser Pro Tyr			
220	660	665	670	
222	cag cct cct ccg cag ccg tat gga cca gtt cct cca gta cct tct			2665
223	Gln Pro Pro Pro Gln Pro Tyr Gly Pro Val Pro Pro Val Pro Ser			
224	675	680	685	
226	gga atg tat gct cct gtg tac gac agc agg cgc atc tgg cgc cca cct			2713
227	Gly Met Tyr Ala Pro Val Tyr Asp Ser Arg Arg Ile Trp Arg Pro Pro			
228	690	695	700	
230	atg tac caa cga gat gac att att aga agc aat tct tta cct cca atg			2761
231	Met Tyr Gln Arg Asp Asp Ile Ile Arg Ser Asn Ser Leu Pro Pro Met			
232	705	710	715	720
234	gat gtg atg cac tca tct gtc tat cag aca tct ttg cgg gaa aga tat			2809
235	Asp Val Met His Ser Ser Val Tyr Gln Thr Ser Leu Arg Glu Arg Tyr			
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238	aac tca tta gat gga tat tat tcg gtg gct tgt cag cca cca agt gag			2857
239	Asn Ser Leu Asp Gly Tyr Tyr Ser Val Ala Cys Gln Pro Pro Ser Glu			
240	740	745	750	
242	cca agg aca act gtg cct tta cca agg gaa cct tgt ggt cat ttg aag			2905
243	Pro Arg Thr Thr Val Pro Leu Pro Arg Glu Pro Cys Gly His Leu Lys			
244	755	760	765	
246	acc agt tgc gag gag cag ata aga aga aag cca gat cag tgg gca cag			2953
247	Thr Ser Cys Glu Glu Gln Ile Arg Arg Lys Pro Asp Gln Trp Ala Gln			
248	770	775	780	
250	tac cac act cag aaa gca cct ctt gtc tct tca act ctt cct gtg gca			3001
251	Tyr His Thr Gln Lys Ala Pro Leu Val Ser Ser Thr Leu Pro Val Ala			
252	785	790	795	800
254	aca cag tca cca aca cca cct tct cct ctg ttc agt gta gac ttt cgt			3049
255	Thr Gln Ser Pro Thr Pro Pro Ser Pro Leu Phe Ser Val Asp Phe Arg			
256	805	810	815	
258	gcg gat ttc tca gag agt gtg agt ggt aca aaa ttt gaa gaa gat cat			3097
259	Ala Asp Phe Ser Glu Ser Val Ser Gly Thr Lys Phe Glu Glu Asp His			
260	820	825	830	
262	ctt tcc cat tat tct ccc tgg tct tgt ggc acc ata ggc tcc tgt ata			3145
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																	860	
270	gtg	tta	atg	gac	ctg	gac	agt	ggt	gat	gtt	aag	aga	aga	gta	cat	tta		3241
271	Val	Leu	Met	Asp	Leu	Asp	Ser	Gly	Asp	Val	Lys	Arg	Arg	Val	His	Leu		
272																	865	
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																	875	
																	880	
274	ttt	gaa	acc	cag	aga	agg	aca	aaa	gaa	gaa	gat	cca	ata	att	ccc	ttt		3289
275	Phe	Glu	Thr	Gln	Arg	Arg	Thr	Lys	Glu	Glu	Asp	Pro	Ile	Ile	Pro	Phe		
276																	885	
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278	agt	gat	gga	ccc	atc	atc	tca	aaa	tgg	ggt	gcg	att	tcc	aga	tct	tcc		3337
279	Ser	Asp	Gly	Pro	Ile	Ile	Ser	Lys	Trp	Gly	Ala	Ile	Ser	Arg	Ser	Ser		
280																	900	
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283	Arg	Thr	Gly	Tyr	His	Thr	Asp	Pro	Val	Gln	Ala	Thr	Ala	Ser	Gln			
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286	gga	agt	gcg	act	aag	ccc	atc	agt	gta	tca	gat	tat	gtc	cct	tat	gtc		3433
287	Gly	Ser	Ala	Thr	Lys	Pro	Ile	Ser	Val	Ser	Asp	Tyr	Val	Pro	Tyr	Val		
288																	930	
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290	aat	gct	gtt	gat	tca	agg	tgg	agt	tca	tat	ggc	aac	gag	gcc	aca	tca		3481
291	Asn	Ala	Val	Asp	Ser	Arg	Trp	Ser	Ser	Tyr	Gly	Asn	Glu	Ala	Thr	Ser		
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294	tca	gca	cac	tat	gtt	gaa	agg	gac	aga	ttc	att	gtt	act	gat	tta	tct		3529
295	Ser	Ala	His	Tyr	Val	Glu	Arg	Asp	Arg	Phe	Ile	Val	Thr	Asp	Leu	Ser		
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																	990	
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303	Gln	Gln	Ala	Lys	Ser	Asn	Ser	Leu	Leu	Leu	Gln	Arg	Glu	Ala	Asn	Ala		
304																	995	
																	1000	
																	1005	
306	ttg	gcc	atg	caa	cag	aag	tgg	aat	tcc	ctg	gat	gaa	ggc	cgt	cac			3670
307	Leu	Ala	Met	Gln	Gln	Lys	Trp	Asn	Ser	Leu	Asp	Glu	Gly	Arg	His			
308																	1010	
																	1015	
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310	ctt	acc	tta	aac	ctt	tta	agc	aag	gaa	att	gaa	cta	aga	aat	gga			3715
311	Leu	Thr	Leu	Asn	Leu	Leu	Ser	Lys	Glu	Ile	Glu	Leu	Arg	Asn	Gly			
312																	1025	
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319	Asp	Arg	Asp	Ile	Glu	Leu	Glu	Leu	Ser	Ala	Leu	Asp	Thr	Asp	Glu			
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323	Pro	Asp	Gly	Gln	Ser	Glu	Pro	Ile	Glu	Glu	Ile	Leu	Asp	Ile	Gln			
324																	1070	
																	1075	
																	1080	
326	ctt	ggc	atc	agt	tct	caa	aat	gat	cag	ttg	cta	aat	gga	atg	gca			3895
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328																	1085	
																	1090	
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330	gtg	gaa	aat	ggg	cat	cca	gta	cag	cag	cac	caa	aag	gag	cca	cca			3940

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